RAW SEQUENCE LISTING ERROR REPORT
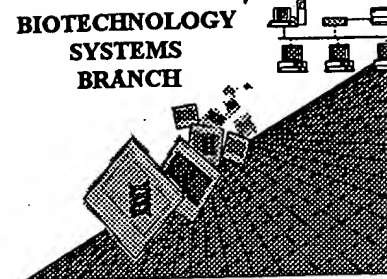
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/580,156_

Art Unit / Team No. : _01PE_

Date Processed by STIC: _6/8/2000_

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT! BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEN WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces:

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING   DATE: 06/08/2000
PATENT APPLICATION: US/09/580,156   TIME: 14:52:03

Input Set : A:\97489us1.app
Output Set: N:\CRF3\06082000\I580156.raw

```
   3 <110> APPLICANT: SANDBERG, LAWRENCE
   4        MITTS, THOMAS F.
   6 <120> TITLE OF INVENTION: ELASTIN PEPTIDE ANALOGS AND USES THEREOF
   8 <130> FILE REFERENCE: 97-489-US-P
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/580,156
C--> 11 <141> CURRENT FILING DATE: 2000-05-30
  13 <150> PRIOR APPLICATION NUMBER: 09/039,308
  14 <151> PRIOR FILING DATE: 1998-03-13
  16 <150> PRIOR APPLICATION NUMBER: PCT/US99/05496
  17 <151> PRIOR FILING DATE: 1999-03-12
  19 <160> NUMBER OF SEQ ID NOS: 54
  21 <170> SOFTWARE: PatentIn Ver. 2.1
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 3
  25 <212> TYPE: PRT
  26 <213> ORGANISM: mammalian
  28 <400> SEQUENCE: 1
  29 Ala Val Gly
  30   1
  33 <210> SEQ ID NO: 2
  34 <211> LENGTH: 4
  35 <212> TYPE: PRT
  36 <213> ORGANISM: mammalian
  38 <400> SEQUENCE: 2
  39 Val Gly Ala Gly
  40   1
  43 <210> SEQ ID NO: 3
  44 <211> LENGTH: 3
  45 <212> TYPE: PRT
  46 <213> ORGANISM: mammalian
  48 <400> SEQUENCE: 3
  49 Ile Gly Gly
  50   1
  53 <210> SEQ ID NO: 4
  54 <211> LENGTH: 2
  55 <212> TYPE: PRT
  56 <213> ORGANISM: mammalian
  58 <400> SEQUENCE: 4
  59 Leu Gly
  60   1
  63 <210> SEQ ID NO: 5
  64 <211> LENGTH: 4
  65 <212> TYPE: PRT
  66 <213> ORGANISM: mammalian
  68 <400> SEQUENCE: 5
  69 Ile Gly Ala Gly
  70   1
```

Does Not Comply
Corrected Diskette Needed

```
 73 <210> SEQ ID NO: 6
 74 <211> LENGTH: 3
 75 <212> TYPE: PRT
 76 <213> ORGANISM: mammalian
 78 <400> SEQUENCE: 6
 79 Leu Gly Gly
 80   1
 83 <210> SEQ ID NO: 7
 84 <211> LENGTH: 4
 85 <212> TYPE: PRT
 86 <213> ORGANISM: mammalian
 88 <400> SEQUENCE: 7
 89 Val Ala Pro Gly
 90   1
 93 <210> SEQ ID NO: 8
 94 <211> LENGTH: 4
 95 <212> TYPE: PRT
 96 <213> ORGANISM: mammalian
 98 <400> SEQUENCE: 8
 99 Leu Gly Pro Gly
100   1
103 <210> SEQ ID NO: 9
104 <211> LENGTH: 4
105 <212> TYPE: PRT
106 <213> ORGANISM: mammalian
108 <400> SEQUENCE: 9
109 Leu Gly Ala Gly
110   1
113 <210> SEQ ID NO: 10
114 <211> LENGTH: 4
115 <212> TYPE: PRT
116 <213> ORGANISM: mammalian
118 <400> SEQUENCE: 10
119 Val Gly Pro Gly
120   1
123 <210> SEQ ID NO: 11
124 <211> LENGTH: 4
125 <212> TYPE: PRT
126 <213> ORGANISM: mammalian
128 <400> SEQUENCE: 11
129 Phe Gly Pro Gly
130   1
133 <210> SEQ ID NO: 12
134 <211> LENGTH: 4
135 <212> TYPE: PRT
136 <213> ORGANISM: mammalian
138 <400> SEQUENCE: 12
139 Val Gly Pro Gln
140   1
```

```
143 <210> SEQ ID NO: 13
144 <211> LENGTH: 3
145 <212> TYPE: PRT
146 <213> ORGANISM: mammalian
148 <400> SEQUENCE: 13
149 Leu Gly Ala
150   1
153 <210> SEQ ID NO: 14
154 <211> LENGTH: 4
155 <212> TYPE: PRT
156 <213> ORGANISM: mammalian
158 <400> SEQUENCE: 14
159 Val Gly Pro Ala
160   1
163 <210> SEQ ID NO: 15
164 <211> LENGTH: 4
165 <212> TYPE: PRT
166 <213> ORGANISM: mammalian
168 <400> SEQUENCE: 15
169 Val Val Pro Gly
170   1
173 <210> SEQ ID NO: 16
174 <211> LENGTH: 4
175 <212> TYPE: PRT
176 <213> ORGANISM: mammalian
178 <400> SEQUENCE: 16
179 Ala Val Pro Gly
180   1
183 <210> SEQ ID NO: 17
184 <211> LENGTH: 4
185 <212> TYPE: PRT
186 <213> ORGANISM: mammalian
188 <400> SEQUENCE: 17
189 Val Val Pro Gln
190   1
193 <210> SEQ ID NO: 18
194 <211> LENGTH: 6
195 <212> TYPE: PRT
196 <213> ORGANISM: mammalian
198 <400> SEQUENCE: 18
199 Val Ala Ala Arg Pro Gly
200   1              5
203 <210> SEQ ID NO: 19
204 <211> LENGTH: 7
205 <212> TYPE: PRT
206 <213> ORGANISM: mammalian
208 <400> SEQUENCE: 19
209 Leu Gly Ala Gly Gly Ala Gly
210   1              5
```

```
213 <210> SEQ ID NO: 20
214 <211> LENGTH: 4
215 <212> TYPE: PRT
216 <213> ORGANISM: mammalian
218 <400> SEQUENCE: 20
219 Ala Ile Pro Gly
220   1
223 <210> SEQ ID NO: 21
224 <211> LENGTH: 5
225 <212> TYPE: PRT
226 <213> ORGANISM: mammalian
228 <400> SEQUENCE: 21   .
229 Leu Gly Pro Gly Gly
230   1               5
233 <210> SEQ ID NO: 22
234 <211> LENGTH: 5
235 <212> TYPE: PRT
236 <213> ORGANISM: mammalian
238 <400> SEQUENCE: 22
239 Ala Ala Ala Gln Ala
240   1               5
243 <210> SEQ ID NO: 23
244 <211> LENGTH: 5
245 <212> TYPE: PRT
246 <213> ORGANISM: mammalian
248 <400> SEQUENCE: 23
W--> 249 Val Gly Val Xaa Gly
250   1               5
253 <210> SEQ ID NO: 24
254 <211> LENGTH: 5
255 <212> TYPE: PRT
256 <213> ORGANISM: mammalian
258 <400> SEQUENCE: 24
259 Val Tyr Pro Gly Gly
260   1               5
263 <210> SEQ ID NO: 25
264 <211> LENGTH: 6
265 <212> TYPE: PRT
266 <213> ORGANISM: mammalian
268 <400> SEQUENCE: 25
269 Ile Gly Gly Val Gly Gly
270   1               5
273 <210> SEQ ID NO: 26
274 <211> LENGTH: 6
275 <212> TYPE: PRT
276 <213> ORGANISM: mammalian
278 <400> SEQUENCE: 26
279 Val Ala Pro Gly Val Gly
280   1               5
```

see item 10 on Erra Summary Sheet

Input Set : A:\97489usl.app
Output Set: N:\CRF3\06082000\I580156.raw

```
283 <210> SEQ ID NO: 27
284 <211> LENGTH: 5
285 <212> TYPE: PRT
286 <213> ORGANISM: mammalian
288 <400> SEQUENCE: 27
289 Leu Gly Val Gly Gly
290    1            5
293 <210> SEQ ID NO: 28
294 <211> LENGTH: 4
295 <212> TYPE: PRT
296 <213> ORGANISM: mammalian
298 <400> SEQUENCE: 28
299 Leu Val Pro Gly
300    1
303 <210> SEQ ID NO: 29
304 <211> LENGTH: 5
305 <212> TYPE: PRT
306 <213> ORGANISM: mammalian
308 <400> SEQUENCE: 29
309 Phe Arg Ala Ala Ala
310    1            5
313 <210> SEQ ID NO: 30
314 <211> LENGTH: 6
315 <212> TYPE: PRT
316 <213> ORGANISM: mammalian
318 <400> SEQUENCE: 30
319 Val Gly Gly Val Pro Gly
320    1            5
323 <210> SEQ ID NO: 31
324 <211> LENGTH: 5
325 <212> TYPE: PRT
326 <213> ORGANISM: mammalian
328 <400> SEQUENCE: 31
329 Phe Gly Pro Gly Gly
330    1            5
333 <210> SEQ ID NO: 32
334 <211> LENGTH: 5
335 <212> TYPE: PRT
336 <213> ORGANISM: mammalian
338 <400> SEQUENCE: 32
339 Val Gly Val Pro Gly
340    1            5
343 <210> SEQ ID NO: 33
344 <211> LENGTH: 6
345 <212> TYPE: PRT
346 <213> ORGANISM: mammalian
348 <400> SEQUENCE: 33
349 Val Leu Pro Gly Ala Gly
350    1            5
```

FYI

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 06/08/2000
PATENT APPLICATION: US/09/580,156   TIME: 14:52:04

Input Set : A:\97489us1.app
Output Set: N:\CRF3\06082000\I580156.raw

```
L:10  M:270 C: Current Application Number differs, Replaced Application Number
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:249 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23
L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:249 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:249 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:359 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:359 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:34
L:359 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
```